

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/913,772A

Source: IFW/6

Date Processed by STIC: 3/4/05

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IFW16

RAW SEQUENCE LISTING

DATE: 03/04/2005

PATENT APPLICATION: US/09/913,772A

TIME: 08:30:18

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03042005\I913772A.raw

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3 <110> APPLICANT: RENNO Toufic
4   BONNEFOY Jean-Yves
6 <120> TITLE OF INVENTION: USE OF AN ENTEROBACTERIUM OmpA PROTEIN ASSOCIATED WITH AN
7   ANTIGEN FOR GENERATING AN ANTIVIRAL, ANTIPARASITIC OR
8   ANTITUMORAL CYTOTOXIC RESPONSE
10 <130> FILE REFERENCE: D 17921
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/913,772A
C--> 13 <141> CURRENT FILING DATE: 2001-09-24
15 <150> PRIOR APPLICATION NUMBER: FR 99 01917
16 <151> PRIOR FILING DATE: 1999-02-17
18 <160> NUMBER OF SEQ ID NOS: 6
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1035
24 <212> TYPE: DNA
25 <213> ORGANISM: Klebsiella pneumoniae
27 <220> FEATURE:
28 <221> NAME/KEY: exon
29 <222> LOCATION: (1)..(1032)
31 <220> FEATURE:
32 <221> NAME/KEY: terminator
33 <222> LOCATION: (1033)..(1035)
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (1)..(1035)
39 <400> SEQUENCE: 1
40 atg aaa gca att ttc gta ctg aat gcg gct ccg aaa gat aac acc tgg      48
41 Met Lys Ala Ile Phe Val Leu Asn Ala Ala Pro Lys Asp Asn Thr Trp
42   1           5           10           15
44 tat gca ggt ggt aaa ctg ggt tgg tcc cag tat cac gac acc ggt ttc      96
45 Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe
46   20           25           30
48 tac ggt aac ggt ttc cag aac aac aac ggt ccg acc cgt aac gat cag      144
49 Tyr Gly Asn Gly Phe Gln Asn Asn Asn Gly Pro Thr Arg Asn Asp Gln
50   35           40           45
52 ctt ggt gct ggt gcg ttc ggt ggt tac cag gtt aac ccg tac ctc ggt      192
53 Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly
54   50           55           60
56 ttc gaa atg ggt tat gac tgg ctg ggc cgt atg gca tat aaa ggc agc      240
57 Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser
58   65           70           75           80
60 gtt gac aac ggt gct ttc aaa gct cag ggc gtt cag ctg acc gct aaa      288
61 Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys

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62	85	90	95	
64	ctg ggt tac ccg atc act gac gat ctg gac atc tac acc cgt ctg ggc	336		
65	Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly			
66	100 105 110			
68	ggc atg gtt tgg cgc gct gac tcc aaa ggc aac tac gct tct acc ggc	384		
69	Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly			
70	115 120 125			
72	gtt tcc cgt agc gaa cac gac act ggc gtt tcc cca gta ttt gct ggc	432		
73	Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly			
74	130 135 140			
76	ggc gta gag tgg gct gtt act cgt gac atc gct acc cgt ctg gaa tac	480		
77	Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr			
78	145 150 155 160			
80	cag tgg gtt aac aac atc ggc gac gcg ggc act gtg ggt acc cgt cct	528		
81	Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro			
82	165 170 175			
84	gat aac ggc atg ctg agc ctg ggc gtt tcc tac cgc ttc ggt cag gaa	576		
85	Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu			
86	180 185 190			
88	gat gct gca ccg gtt gtt gct ccg gct ccg gct ccg gct ccg gaa gtg	624		
89	Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Ala Pro Glu Val			
90	195 200 205			
92	gct acc aag cac ttc acc ctg aag tct gac gtt ctg ttc aac ttc aac	672		
93	Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn			
94	210 215 220			
96	aaa gct acc ctg aaa ccg gaa ggt cag cag gct ctg gat cag ctg tac	720		
97	Lys Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr			
98	225 230 235 240			
100	act cag ctg agc aac atg gat ccg aaa gac ggt tcc gct gtt gtt ctg	768		
101	Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Val Leu			
102	245 250 255			
104	ggc tac acc gac cgc atc ggt tcc gaa gct tac aac cag cag ctg tct	816		
105	Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser			
106	260 265 270			
108	gag aaa cgt gct cag tcc gtt gtt gac tac ctg gtt gct aaa ggc atc	864		
109	Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile			
110	275 280 285			
112	ccg gct ggc aaa atc tcc gct cgc ggc atg ggt gaa tcc aac ccg gtt	912		
113	Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val			
114	290 295 300			
116	act ggc aac acc tgt gac aac gtg aaa gct cgc gct gcc ctg atc gat	960		
117	Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp			
118	305 310 315 320			
120	tgc ctg gct ccg gat cgt cgt gta gag atc gaa gtt aaa ggc tac aaa	1008		
121	Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys			
122	325 330 335			
124	gaa gtt gta act cag ccg gcg ggt taa	1035		
125	Glu Val Val Thr Gln Pro Ala Gly			
126	340			

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129 <210> SEQ ID NO: 2
130 <211> LENGTH: 344
131 <212> TYPE: PRT
132 <213> ORGANISM: Klebsiella pneumoniae
134 <400> SEQUENCE: 2
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136 1 5 10 15
138 Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe
139 20 25 30
141 Tyr Gly Asn Gly Phe Gln Asn Asn Asn Gly Pro Thr Arg Asn Asp Gln
142 35 40 45
144 Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly
145 50 55 60
147 Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser
148 65 70 75 80
150 Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys
151 85 90 95
153 Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly
154 100 105 110
156 Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly
157 115 120 125
159 Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly
160 130 135 140
162 Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr
163 145 150 155 160
165 Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro
166 165 170 175
168 Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu
169 180 185 190
171 Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Ala Pro Glu Val
172 195 200 205
174 Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn
175 210 215 220
177 Lys Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr
178 225 230 235 240
180 Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Val Leu
181 245 250 255
183 Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser
184 260 265 270
186 Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile
187 275 280 285
189 Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val
190 290 295 300
192 Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp
193 305 310 315 320
195 Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys
196 325 330 335
198 Glu Val Val Thr Gln Pro Ala Gly
199 340

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203 <210> SEQ ID NO: 3
204 <211> LENGTH: 10
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Peptide derived from the Mart-1/MelanA antigen expressed by
210 melanoma cells.
212 <400> SEQUENCE: 3
213 Glu Leu Ala Gly Ile Gly Ile Leu Thr Val
214 1 5 10
217 <210> SEQ ID NO: 4
218 <211> LENGTH: 8
219 <212> TYPE: PRT
220 <213> ORGANISM: Homo sapiens
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Derivative of tyrosinase-related protein 2 (TRP-2).
225 <400> SEQUENCE: 4
226 Val Tyr Asp Phe Phe Val Trp Leu
227 1 5
237 <210> SEQ ID NO: 5
238 <211> LENGTH: 9
239 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Peptide derived from the Mart-1/MelanA antigen expressed by
244 melanoma cells.
246 <400> SEQUENCE: 5
247 Ala Ala Gly Ile Gly Ile Leu Thr Val
248 1 5
252 <210> SEQ ID NO: 6
253 <211> LENGTH: 10
254 <212> TYPE: PRT
255 <213> ORGANISM: Homo sapiens
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Peptide derived from the Mart-1/MelanA antigen expressed by
259 melanoma cells.
261 <400> SEQUENCE: 6
262 Glu Ala Ala Gly Ile Gly Ile Leu Thr Val
263 1 5 10

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VERIFICATION SUMMARY

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Input Set : A:\PTO.SR.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date